What is claimed is:

1. A method of identifying one or more markers for Alzheimer's Disease, wherein each of said one or more markers corresponds to a gene transcript, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having Alzheimer's Disease, wherein each of said one or more transcripts is expressed by a gene that is a candidate marker for Alzheimer's Disease; and

b) comparing the level of each of said one or more gene transcripts from said step a) with the level of each of said one or more genes transcripts in blood obtained from one or more individuals not having Alzheimer's Disease,

wherein those compared transcripts which display differing levels in the comparison of step b) are identified as being markers for Alzheimer's Disease.

2. A method of identifying one or more markers for Alzheimer's Disease, wherein each of said one or more markers corresponds to a gene transcript, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having Alzheimer's Disease, wherein each of said one or more transcripts is expressed by a gene that is a candidate marker for Alzheimer's Disease; and

b) comparing the level of each of said one or more gene transcripts from said step a) with the level of each of said one or more genes transcripts in blood obtained from one or more individuals having Alzheimer's Disease,

wherein those compared transcripts which display the same levels in the comparison of step b) are identified as being markers for Alzheimer's Disease.

3. A method of identifying one or more markers of a stage of Alzheimer's Disease progression or regression, wherein each of said one or more markers corresponds to a gene transcript, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having a stage of Alzheimer's Disease, wherein said one or more individuals are at the same progressive or regressive stage of Alzheimer's Disease, and wherein each of said one or more transcripts is expressed by a gene that is a candidate

marker for determining the stage of progression or regression of Alzheimer's Disease, and;

b) comparing the level of each of said one or more gene transcripts from said step a) with the level of each of said one or more genes transcripts in blood obtained from one or more individuals who are at a progressive or regressive stage of Alzheimer's Disease distinct from that of said one or more individuals of step a),

wherein those compared transcripts which display differing levels in the comparison of step b) are identified as being markers for the stage of progression or regression of Alzheimer's Disease.

4. A method of identifying one or more markers of a stage of Alzheimer's Disease progression or regression, wherein each of said one or more markers corresponds to a gene transcript, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having a stage of Alzheimer's Disease, wherein said one or more individuals are at the same progressive or regressive stage of Alzheimer's Disease, and wherein each of said one or more transcripts is expressed by a gene that is a candidate marker for determining the stage of progression or regression of Alzheimer's Disease, and;

b) comparing the level of each of said one or more gene transcripts from said step a) with the level of each of said one or more genes transcripts in blood obtained from one or more individuals who are at a progressive or regressive stage of Alzheimer's Disease identical to that of said one or more individuals of step a),

wherein those compared transcripts which display the same levels in the comparison of step b) are identified as being markers for the stage of progression or regression of Alzheimer's Disease.

5. The method of any one of claims 1 - 4, wherein each of said one or more markers identifies one or more transcripts of one or more non immune response genes.

6. The method of any one of claims 1 - 4, wherein each of said one or more markers identifies a transcript of a gene expressed by non-blood tissue.

7. The method of any one of claims 1 - 4, wherein each of said one or more markers identifies a transcript of a gene expressed by non-lymphoid tissue.

8. The method of any one of claims 1 - 4, wherein said one marker of said one or more markers identifies the sequence of amyloid precursor protein (APP).

9. A method of diagnosing or prognosing Alzheimer's Disease in an individual, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from said individual, wherein said one or more gene transcripts corresponds to said one or more markers of claim 1 and claim 2, and

b) comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals not having Alzheimer's Disease,

wherein detecting a difference in the levels of each of said one or more gene transcripts in the comparison of step b) is indicative of Alzheimer's Disease in the individual of step a).

10. A method of diagnosing or prognosing Alzheimer's Disease in an individual, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from said individual, wherein said one or more gene transcripts correspond to said one or more markers of claim 1 and claim 2 and

b) comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals having Alzheimer's Disease,

wherein detecting the same levels of each of said one or more gene transcripts in the comparison of step b) is indicative of Alzheimer's Disease in the individual of step a).

11. A method of determining a stage of disease progression or regression in an individual having Alzheimer's Disease, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from said individual having Alzheimer's Disease, wherein said one or more gene transcripts correspond to said one or more markers of claim 3 and claim 4, and

b) comparing the level of each if said one or more gene transcripts in said blood

according to step a) with the level of each of said one or more gene transcripts in blood obtained from one or more individuals who each have been diagnosed as being at the same progressive or regressive stage of Alzheimer's Disease,

wherein the comparison from step b) allows the determination of the stage of Alzheimer's Disease progression or regression in the individual of step a).

12. A method of diagnosing or prognosing Alzheimer's Disease in an individual, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from said individual, wherein said one or more gene transcripts correspond to said one or more markers of claim 1 and claim 2, and

b) comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals having Alzheimer's Disease,

c) comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals not having Alzheimer's Disease,

d) determining whether the level of said one or more gene transcripts of step a) classify with the levels of said transcripts in step b) as compared with levels of said transcripts in step c),

wherein said determination is indicative of said individual of step a) having Alzheimer's Disease.

13. A method of determining a stage of disease progression or regression in an individual having Alzheimer's Disease, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from said individual having Alzheimer's Disease, wherein said one or more gene transcripts correspond to said one or more markers of claim 3 and claim 4, and

b) comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals having said stage of Alzheimer's Disease,

c) comparing the level of each of said one or more gene transcripts in said blood

according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals not having said stage of Alzheimer's Disease,

d) determining whether the level of said one or more gene transcripts of step a) classify with the levels of said transcripts in step b) as compared with levels of said transcripts in step c),

wherein said determination is indicative of said individual of step a) having said stage of Alzheimer's Disease.

14. The method of any one of claims 1 - 4 and 9 - 13, wherein said one or more gene transcripts are transcribed from one or more genes selected from the group consisting of:

a) non-immune response genes,

b) genes expressed by non blood tissue, and

c) genes expressed by non lymphoid tissue.

15. The method of any one of claims 1 - 4 and 9 - 13, wherein said blood comprises a blood sample obtained from said one or more individuals.

16. The method of claim 15, wherein said blood sample consists of whole blood.

17. The method of claim 15, wherein said blood sample consists of a drop of blood.

18. The method of claim 15, wherein said blood sample consists of blood that has been lysed.

19. The method of claim 15, further comprising the step of isolating RNA from said blood samples.

20. The method of any one of claims 1 - 4 and 9 - 13, wherein the step of determining the level of each of said one or more gene transcripts comprises quantitative RT-PCR (QRT-PCR), wherein said one or more transcripts are from step a) and/or step b) of claims 1 - 4 and 9 - 13.

21. The method of claim 20, wherein said QRT-PCR comprises primers which hybridize to said one or more transcripts or the complement thereof, wherein said one or more transcripts are from step a) and/or step b) of claims 1 - 4 and 9 - 13.

22. The method of claim 20, wherein said primers are 15-25 nucleotides in length.

23. The method of any one of claims 1 - 4 and 9 - 13, wherein the step of determining the level of each of said one or more gene transcripts comprises hybridizing a first plurality of isolated nucleic acid molecules that correspond to said one or more transcripts, to an array comprising a second plurality of isolated nucleic acid molecules.

24. The method of claim 23, wherein said first plurality of isolated nucleic acid molecules comprises RNA, DNA, cDNA, PCR products or ESTs.

25. The method of claim 23, wherein said array comprises a plurality of isolated nucleic acid molecules comprising RNA, DNA, cDNA, PCR products or ESTs.

26. The method of claim 25, wherein said array comprises two or more of the markers of claim 1.

27. The method of claim 25, wherein said array comprises two or more of the markers of claim 2.

28. The method of claim 25, wherein said array comprises two or more of the markers of claim 3.

29. The method of claim 25, wherein said array comprises two or more of the markers of claim 4.

30. The method of claim 25, wherein said array comprises a plurality of nucleic acid molecules that correspond to genes of the human genome.

31. A plurality of isolated nucleic acid molecules that correspond to two or more of the markers of claim 1.

32. A plurality of isolated nucleic acid molecules that correspond to two or more of the markers of claim 2.

33. A plurality of isolated nucleic acid molecules that correspond to two or more of the markers of claim 3.

34. A plurality of isolated nucleic acid molecules that correspond to two or more of the markers of claim 4.

35. The method of claim 24, wherein said ESTs comprise a length of greater than 100 nucleotides.

36. An array consisting essentially of the plurality of nucleic acid molecules of claim 31.

37. An array consisting essentially of the plurality of nucleic acid molecules of claim 32.

38. An array consisting essentially of the plurality of nucleic acid molecules of claim 33.

39. An array consisting essentially of the plurality of nucleic acid molecules of claim 34.

40. A kit for diagnosing or prognosing Alzheimer's Disease comprising:

a) two gene-specific priming means designed to produce double stranded DNA complementary to a gene that corresponds to a marker selected from the group consisting of the markers of claim 1, claim 2, claim 3 and claim 4 wherein said first priming means contains a sequence which can hybridize to RNA, cDNA or an EST complementary to said gene to create an extension product and said second priming means capable of hybridizing to said extension product;

b) an enzyme with reverse transcriptase activity,

c) an enzyme with thermostable DNA polymerase activity, and

d) a labeling means;

wherein said primers are used to detect the quantitative expression levels of said gene in a test subject.

41. A kit for monitoring a course of therapeutic treatment of Alzheimer's Disease, comprising:

a) two gene-specific priming means designed to produce double stranded DNA complementary to a gene that corresponds to a marker selected from the group consisting of the markers of claim 1, claim 2, claim 3 and claim 4; wherein said first priming means contains a sequence which can hybridize to RNA, cDNA or an EST complementary to said gene to create an extension product and said second priming means capable of hybridizing

to said extension product;

b) an enzyme with reverse transcriptase activity,

c) an enzyme with thermostable DNA polymerase activity, and

d) a labeling means;

wherein said primers are used to detect the quantitative expression levels of said gene in a test subject.

42. A kit for monitoring progression or regression of Alzheimer's Disease, comprising:

a) two gene-specific priming means designed to produce double stranded DNA complementary to a gene that corresponds to a marker selected from the group consisting of the markers of claim 1, claim 2, claim 3 and claim 4, wherein said first priming means contains a sequence which can hybridize to RNA, cDNA or an EST complementary to said gene to create an extension product and said second priming means capable of hybridizing to said extension product;

b) an enzyme with reverse transcriptase activity,

c) an enzyme with thermostable DNA polymerase activity, and

d) a labeling means;

wherein said primers are used to detect the quantitative expression levels of said gene in a test subject.

43. The method of claim 25, wherein said ESTs comprise a length greater than 100 nucleotides.